

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/534, 386
Source: PLT
Date Processed by STIC: 02/16/2006

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PCT

RAW SEQUENCE LISTING

DATE: 02/16/2006

PATENT APPLICATION: US/10/534,386

TIME: 13:50:24

Input Set : E:\406uspc.app.txt

Output Set: N:\CRF4\02162006\J534386.raw

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3 <110> APPLICANT: Nakauchi, Hiromitsu
4      Iwama, Atsushi
6 <120> TITLE OF INVENTION: EXPANSION AGENTS FOR STEM CELLS
8 <130> FILE REFERENCE: 790086.406USPC
10 <140> CURRENT APPLICATION NUMBER: US 10/534,386
C--> 11 <141> CURRENT FILING DATE: 2005-05-06
13 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/013579
14 <151> PRIOR FILING DATE: 2003-10-23
16 <150> PRIOR APPLICATION NUMBER: JP 2002-326190
17 <151> PRIOR FILING DATE: 2002-11-08
19 <160> NUMBER OF SEQ ID NOS: 13
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 2385
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(2385)
31 <223> OTHER INFORMATION:
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36 1      5      10      15
38 cag atg cag gtg ctg tac ggc cag cac ttc ccc atc gag gtc cgg cac      96
39 Gln Met Gln Val Leu Tyr Gly Gln His Phe Pro Ile Glu Val Arg His
40      20      25      30
42 tac ttg gcc cag tgg att gag agc cag cca tgg gat gcc att gac ttg      144
43 Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp Asp Ala Ile Asp Leu
44      35      40      45
46 gac aat ccc cag gac aga gcc caa gcc acc cag ctc ctg gag ggc ctg      192
47 Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln Leu Leu Glu Gly Leu
48      50      55      60
50 gtg cag gag ctg cag aag aag gcg gag cac cag gtg ggg gaa gat ggg      240
51 Val Gln Glu Leu Gln Lys Lys Ala Glu His Gln Val Gly Glu Asp Gly
52 65      70      75      80
54 ttt tta ctg aag atc aag ctg ggg cac tac gcc acg cag ctc cag aaa      288
55 Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala Thr Gln Leu Gln Lys
56      85      90      95
58 aca tat gac cgc tgc ccc ctg gag ctg gtc cgc tgc atc cgg cac att      336
59 Thr Tyr Asp Arg Cys Pro Leu Glu Leu Val Arg Cys Ile Arg His Ile
60      100      105      110
62 ctg tac aat gaa cag agg ctg gtc cga gaa gcc aac aat tgc agc tct      384

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66 ccg gct ggg atc ctg gtt gac gcc atg tcc cag aag cac ctt cag atc      432
67 Pro Ala Gly Ile Leu Val Asp Ala Met Ser Gln Lys His Leu Gln Ile
68      130      135      140
70 aac cag aca ttt gag gag ctg cga ctg gtc acg cag gac aca gag aat      480
71 Asn Gln Thr Phe Glu Glu Leu Arg Leu Val Thr Gln Asp Thr Glu Asn
72 145      150      155      160
74 gag ctg aag aaa ctg cag cag act cag gag tac ttc atc atc cag tac      528
75 Glu Leu Lys Lys Leu Gln Gln Thr Gln Glu Tyr Phe Ile Ile Gln Tyr
76      165      170      175
78 cag gag agc ctg agg atc caa gct cag ttt gcc cag ctg gcc cag ctg      576
79 Gln Glu Ser Leu Arg Ile Gln Ala Gln Phe Ala Gln Leu Ala Gln Leu
80      180      185      190
82 agc ccc cag gag cgt ctg agc cgg gag acg gcc ctc cag cag aag cag      624
83 Ser Pro Gln Glu Arg Leu Ser Arg Glu Thr Ala Leu Gln Gln Lys Gln
84      195      200      205
86 gtg tct ctg gag gcc tgg ttg cag cgt gag gca cag aca ctg cag cag      672
87 Val Ser Leu Glu Ala Trp Leu Gln Arg Glu Ala Gln Thr Leu Gln Gln
88      210      215      220
90 tac cgc gtg gag ctg gcc gag aag cac cag aag acc ctg cag ctg ctg      720
91 Tyr Arg Val Glu Leu Ala Glu Lys His Gln Lys Thr Leu Gln Leu Leu
92 225      230      235      240
94 cgg aag cag cag acc atc atc ctg gat gac gag ctg atc cag tgg aag      768
95 Arg Lys Gln Gln Thr Ile Ile Leu Asp Asp Glu Leu Ile Gln Trp Lys
96      245      250      255
98 cgg cgg cag cag ctg gcc ggg aac ggc ggg ccc ccc gag ggc agc ctg      816
99 Arg Arg Gln Gln Leu Ala Gly Asn Gly Gly Pro Pro Glu Gly Ser Leu
100      260      265      270
102 gac gtg cta cag tcc tgg tgt gag aag ttg gcc gag atc atc tgg cag      864
103 Asp Val Leu Gln Ser Trp Cys Glu Lys Leu Ala Glu Ile Ile Trp Gln
104      275      280      285
106 aac cgg cag cag atc cgc agg gct gag cac ctc tgc cag cag ctg ccc      912
107 Asn Arg Gln Gln Ile Arg Arg Ala Glu His Leu Cys Gln Gln Leu Pro
108      290      295      300
110 atc ccc ggc cca gtg gag gag atg ctg gcc gag gtc aac gcc acc atc      960
111 Ile Pro Gly Pro Val Glu Glu Met Leu Ala Glu Val Asn Ala Thr Ile
112 305      310      315      320
114 acg gac att atc tca gcc ctg gtg acc agc aca ttc atc att gag aag      1008
115 Thr Asp Ile Ile Ser Ala Leu Val Thr Ser Thr Phe Ile Ile Glu Lys
116      325      330      335
118 cag cct cct cag gtc ctg aag acc cag acc aag ttt gca gcc acc gta      1056
119 Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys Phe Ala Ala Thr Val
120      340      345      350
122 cgc ctg ctg gtg ggc ggg aag ctg aac gtg cac atg aat ccc ccc cag      1104
123 Arg Leu Leu Val Gly Gly Lys Leu Asn Val His Met Asn Pro Pro Gln
124      355      360      365
126 gtg aag gcc acc atc atc agt gag cag cag gcc aag tct ctg ctt aaa      1152
127 Val Lys Ala Thr Ile Ile Ser Glu Gln Gln Ala Lys Ser Leu Leu Lys

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130	aat gag aac acc cgc aac gag tgc agt ggt gag atc ctg aac aac tgc	1200		
131	Asn Glu Asn Thr Arg Asn Glu Cys Ser Gly Glu Ile Leu Asn Asn Cys			
132	385 390 395 400			
134	tgc gtg atg gag tac cac caa gcc acg ggc acc ctc agt gcc cac ttc	1248		
135	Cys Val Met Glu Tyr His Gln Ala Thr Gly Thr Leu Ser Ala His Phe			
136	405 410 415			
138	agg aac atg tca ctg aag agg atc aag cgt gct gac cgg cgg ggt gca	1296		
139	Arg Asn Met Ser Leu Lys Arg Ile Lys Arg Ala Asp Arg Arg Gly Ala			
140	420 425 430			
142	gag tcc gtg aca gag gag aag ttc aca gtc ctg ttt gag tct cag ttc	1344		
143	Glu Ser Val Thr Glu Glu Lys Phe Thr Val Leu Phe Glu Ser Gln Phe			
144	435 440 445			
146	agt gtt ggc agc aat gag ctt gtg ttc cag gtg aag act ctg tcc cta	1392		
147	Ser Val Gly Ser Asn Glu Leu Val Phe Gln Val Lys Thr Leu Ser Leu			
148	450 455 460			
150	cct gtg gtt gtc atc gtc cac ggc agc cag gac cac aat gcc acg gct	1440		
151	Pro Val Val Val Ile Val His Gly Ser Gln Asp His Asn Ala Thr Ala			
152	465 470 480			
154	act gtg ctg tgg gac aat gcc ttt gct gag ccg ggc agg gtg cca ttt	1488		
155	Thr Val Leu Trp Asp Asn Ala Phe Ala Glu Pro Gly Arg Val Pro Phe			
156	485 490 495			
158	gcc gtg cct gac aaa gtg ctg tgg ccg cag ctg tgt gag gcg ctc aac	1536		
159	Ala Val Pro Asp Lys Val Leu Trp Pro Gln Leu Cys Glu Ala Leu Asn			
160	500 505 510			
162	atg aaa ttc aag gcc gaa gtg cag agc aac cgg ggc ctg acc aag gag	1584		
163	Met Lys Phe Lys Ala Glu Val Gln Ser Asn Arg Gly Leu Thr Lys Glu			
164	515 520 525			
166	aac ctc gtg ttc ctg gcg cag aaa ctg ttc aac aac agc agc agc cac	1632		
167	Asn Leu Val Phe Leu Ala Gln Lys Leu Phe Asn Asn Ser Ser Ser His			
168	530 535 540			
170	ctg gag gac tac agt ggc ctg tcc gtg tcc tgg tcc cag ttc aac agg	1680		
171	Leu Glu Asp Tyr Ser Gly Leu Ser Val Ser Trp Ser Gln Phe Asn Arg			
172	545 550 555 560			
174	gag aac ttg ccg ggc tgg aac tac acc ttc tgg cag tgg ttt gac ggg	1728		
175	Glu Asn Leu Pro Gly Trp Asn Tyr Thr Phe Trp Gln Trp Phe Asp Gly			
176	565 570 575			
178	gtg atg gag gtg ttg aag aag cac cac aag ccc cac tgg aat gat ggg	1776		
179	Val Met Glu Val Leu Lys Lys His His Lys Pro His Trp Asn Asp Gly			
180	580 585 590			
182	gcc atc cta ggt ttt gtg aat aag caa cag gcc cac gac ctg ctc atc	1824		
183	Ala Ile Leu Gly Phe Val Asn Lys Gln Gln Ala His Asp Leu Leu Ile			
184	595 600 605			
186	aac aag ccc gac ggg acc ttc ttg ttg cgc ttt agt gac tca gaa atc	1872		
187	Asn Lys Pro Asp Gly Thr Phe Leu Leu Arg Phe Ser Asp Ser Glu Ile			
188	610 615 620			
190	ggg ggc atc acc atc gcc tgg aag ttt gac tcc ccg gaa cgc aac ctg	1920		
191	Gly Gly Ile Thr Ile Ala Trp Lys Phe Asp Ser Pro Glu Arg Asn Leu			
192	625 630 635 640			

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194 tgg aac ctg aaa cca ttc acc acg cgg gat ttc tcc atc agg tcc ctg      1968
195 Trp Asn Leu Lys Pro Phe Thr Thr Arg Asp Phe Ser Ile Arg Ser Leu
196                               645                               650                               655
198 gct gac cgg ctg ggg gac ctg agc tat ctc atc tat gtg ttt cct gac      2016
199 Ala Asp Arg Leu Gly Asp Leu Ser Tyr Leu Ile Tyr Val Phe Pro Asp
200                               660                               665                               670
202 cgc ccc aag gat gag gtc ttc tcc aag tac tac act cct gtg ctg gct      2064
203 Arg Pro Lys Asp Glu Val Phe Ser Lys Tyr Tyr Thr Pro Val Leu Ala
204                               675                               680                               685
206 aaa gct gtt gat gga tat gtg aaa cca cag atc aag caa gtg gtc cct      2112
207 Lys Ala Val Asp Gly Tyr Val Lys Pro Gln Ile Lys Gln Val Val Pro
208                               690                               695                               700
210 gag ttt gtg aat gca tct gca gat gct ggg ggc agc agc gcc acg tac      2160
211 Glu Phe Val Asn Ala Ser Ala Asp Ala Gly Gly Ser Ser Ala Thr Tyr
212 705                               710                               715                               720
214 atg gac cag gcc ccc tcc cca gct gtg tgc ccc cag gct ccc tat aac      2208
215 Met Asp Gln Ala Pro Ser Pro Ala Val Cys Pro Gln Ala Pro Tyr Asn
216                               725                               730                               735
218 atg tac cca cag aac cct gac cat gta ctc gat cag gga gaa ttc      2256
219 Met Tyr Pro Gln Asn Pro Asp His Val Leu Asp Gln Asp Gly Glu Phe
220                               740                               745                               750
222 gac ctg gat gag acc atg gat gtg gcc agg cac gtg gag gaa ctc tta      2304
223 Asp Leu Asp Glu Thr Met Asp Val Ala Arg His Val Glu Glu Leu Leu
224                               755                               760                               765
226 cgc cga cca atg gac agt ctt gac tcc cgc ctc tcg ccc cct gcc ggt      2352
227 Arg Arg Pro Met Asp Ser Leu Asp Ser Arg Leu Ser Pro Pro Ala Gly
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232 785                               790
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236 <211> LENGTH: 794
237 <212> TYPE: PRT
238 <213> ORGANISM: Homo sapiens
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247                               20                               25                               30
250 Tyr Leu Ala Gln Trp Ile Glu Ser Gln Pro Trp Asp Ala Ile Asp Leu
251                               35                               40                               45
255 Asp Asn Pro Gln Asp Arg Ala Gln Ala Thr Gln Leu Leu Glu Gly Leu
256                               50                               55                               60
259 Val Gln Glu Leu Gln Lys Lys Ala Glu His Gln Val Gly Glu Asp Gly
260 65                               70                               75                               80
263 Phe Leu Leu Lys Ile Lys Leu Gly His Tyr Ala Thr Gln Leu Gln Lys
264                               85                               90                               95
267 Thr Tyr Asp Arg Cys Pro Leu Glu Leu Val Arg Cys Ile Arg His Ile
268                               100                               105                               110

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271 Leu Tyr Asn Glu Gln Arg Leu Val Arg Glu Ala Asn Asn Cys Ser Ser
272      115      120      125
275 Pro Ala Gly Ile Leu Val Asp Ala Met Ser Gln Lys His Leu Gln Ile
276      130      135      140
279 Asn Gln Thr Phe Glu Glu Leu Arg Leu Val Thr Gln Asp Thr Glu Asn
280 145      150      155      160
283 Glu Leu Lys Lys Leu Gln Gln Thr Gln Glu Tyr Phe Ile Ile Gln Tyr
284      165      170      175
287 Gln Glu Ser Leu Arg Ile Gln Ala Gln Phe Ala Gln Leu Ala Gln Leu
288      180      185      190
291 Ser Pro Gln Glu Arg Leu Ser Arg Glu Thr Ala Leu Gln Gln Lys Gln
292      195      200      205
295 Val Ser Leu Glu Ala Trp Leu Gln Arg Glu Ala Gln Thr Leu Gln Gln
296      210      215      220
299 Tyr Arg Val Glu Leu Ala Glu Lys His Gln Lys Thr Leu Gln Leu Leu
300 225      230      235      240
303 Arg Lys Gln Gln Thr Ile Ile Leu Asp Asp Glu Leu Ile Gln Trp Lys
304      245      250      255
307 Arg Arg Gln Gln Leu Ala Gly Asn Gly Gly Pro Pro Glu Gly Ser Leu
308      260      265      270
311 Asp Val Leu Gln Ser Trp Cys Glu Lys Leu Ala Glu Ile Ile Trp Gln
312      275      280      285
315 Asn Arg Gln Gln Ile Arg Arg Ala Glu His Leu Cys Gln Gln Leu Pro
316      290      295      300
319 Ile Pro Gly Pro Val Glu Glu Met Leu Ala Glu Val Asn Ala Thr Ile
320 305      310      315      320
323 Thr Asp Ile Ile Ser Ala Leu Val Thr Ser Thr Phe Ile Ile Glu Lys
324      325      330      335
327 Gln Pro Pro Gln Val Leu Lys Thr Gln Thr Lys Phe Ala Ala Thr Val
328      340      345      350
331 Arg Leu Leu Val Gly Gly Lys Leu Asn Val His Met Asn Pro Pro Gln
332      355      360      365
335 Val Lys Ala Thr Ile Ile Ser Glu Gln Gln Ala Lys Ser Leu Leu Lys
336      370      375      380
339 Asn Glu Asn Thr Arg Asn Glu Cys Ser Gly Glu Ile Leu Asn Asn Cys
340 385      390      395      400
343 Cys Val Met Glu Tyr His Gln Ala Thr Gly Thr Leu Ser Ala His Phe
344      405      410      415
347 Arg Asn Met Ser Leu Lys Arg Ile Lys Arg Ala Asp Arg Arg Gly Ala
348      420      425      430
351 Glu Ser Val Thr Glu Glu Lys Phe Thr Val Leu Phe Glu Ser Gln Phe
352      435      440      445
355 Ser Val Gly Ser Asn Glu Leu Val Phe Gln Val Lys Thr Leu Ser Leu
356      450      455      460
359 Pro Val Val Val Ile Val His Gly Ser Gln Asp His Asn Ala Thr Ala
360 465      470      475      480
363 Thr Val Leu Trp Asp Asn Ala Phe Ala Glu Pro Gly Arg Val Pro Phe
364      485      490      495
367 Ala Val Pro Asp Lys Val Leu Trp Pro Gln Leu Cys Glu Ala Leu Asn

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VERIFICATION SUMMARY

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Input Set : E:\406uspc.app.txt

Output Set: N:\CRF4\02162006\J534386.raw

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L:455 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:453
L:875 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:873
L:1295 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:1293
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